



#14

SEQUENCE LISTING

<110> MAX-PLANCK-GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN E.V.
NATIONAL PUBLIC HEALTH INSTITUTE
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PERHEENTUPA, Jaakko
PALOTIE, Aarno
HORELLI-KUITUNEN, Nina
YASPO, Marie-Laure
LEHRACH, Hans

<120> NUCLEIC ACID MOLECULE ENCODING A (POLY)PEPTIDE CO-SEGREGATING IN
MUTATED FORM WITH AUTOIMMUNE POLYENDOCRINOPATHY CANDIDIASIS ECTODERMAL
DYSTROPHY (APECED)

<130> VOSS1130

<140> US 09/509,595

<141> 2000-07-05

<150> EP 97117154.1

<151> 1997-10-02

<150> EP 97117398.4

<151> 1997-10-08

<150> EP 97119810.6

<151> 1997-11-12

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<170> PatentIn version 3.1

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atg gcg acg gac gcg gcg cta cgc cgg ctt ctg agg ctg cac cgc acg 168

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Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His

35 40 45

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Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val	
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Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu	
115 120 125	
ccc acc aag agg aag gcc tca gaa gag gct cga gct gcc gcg cca gca	552
Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala	
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Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro	
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cct ggg cct gcc aag gat gac act gcc agt cac gag ccc gct ctg cac	1656
Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His	
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Arg Asp Asp Leu Glu Ser Leu Ser Glu His Thr Phe Asp Gly Ile	
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Ser		tgagaaggac	
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		gacaccagcc atcatgtgcc	
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tggtgacct	ctaaaaatat	aaaaattagc tgggtgtggg	2048
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gctacatggg	agcctgaggc	atgagaatca cttgaactcg	2108
		ggagggtggag gttgcagtga	
gctgagattg	cgccactgca	ctccagtctg gtcggcaaga	2168
		gtgagactcc gtctcaaaaa	
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Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
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Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
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115 120 125

Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala
 130 135 140

Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala
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Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro
 165 170 175

Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val
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Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly
 195 200 205

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Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly
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 245 250 255

Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg
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Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp
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Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp
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Ser
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Thr Glu Ile Ala Val Ala Ile Asp Ser Ala Phe Pro Leu Leu His Ala
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cta gcc gac cac gac gtg gtc cct gag gac aag ttc cag gag acg ctc 144
Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu
35 40 45
cgt ctg aag gag aag gaa ggc tgc ccc cag gcc ttc cac gcc ctg ctg 192
Arg Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu
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Ile Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Ser Arg Leu His Ser

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Pro Pro Thr Lys Arg Lys Ala Leu Glu Glu Pro Arg Ala Thr Pro Pro
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Ala Thr Leu Ala Ser Lys Ser Val Ser Ser Pro Gly Ser His Leu Lys
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Pro Leu Gly Asn Gly Ile Gln Thr Met Ala Ala Ser Val Gln Arg Ala
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Gln Lys Val Gly Gln Gln Cys Gly Val Pro Pro Leu Pro Ser Leu Pro						
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Ser Glu Pro Gln Val Asn Gln Lys Asn Glu Asp Glu Cys Ala Val Cys						
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His Leu Ala Cys Leu Ser Pro Pro Leu Gln Glu Ile Pro Ser Gly Leu						
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Trp Arg Cys Ser Cys Cys Leu Gln Gly Arg Val Gln Gln Asn Leu Ser						
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Gln Pro Glu Val Ser Arg Pro Pro Glu Leu Pro Ala Glu Thr Pro Ile						
	355		360			365
Leu Val Gly Leu Arg Ser Ala Ser Glu Lys Thr Arg Gly Pro Ser Arg						
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Glu Leu Lys Ala Ser Ser Asp Ala Ala Val Thr Tyr Val Asn Leu Leu						
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Ala Pro His Pro Ala Ala Pro Leu Leu Glu Pro Ser Ala Leu Cys Pro						
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Leu Leu Ser Ala Gly Asn Glu Gly Arg Pro Gly Pro Ala Pro Ser Ala						
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Arg Cys Ser Val Cys Gly Asp Gly Thr Glu Val Leu Arg Cys Ala His						
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Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Thr Ala Ala Ala						
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Arg Pro Gly Thr Asn Leu Arg Cys Lys Ser Cys Ser Ala Asp Ser Thr						
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Pro Val Leu His Arg Asp Asp Leu Glu Ser Leu Leu Asn Glu His Ser
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Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
 35 40 45

Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
 50 55 60

Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
 65 70 75 80

Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile
 85 90 95

Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
 100 105 110

Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu
 115 120 125

Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala
 130 135 140

Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala
 145 150 155 160

Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro
 165 170 175

Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val
 180 185 190

Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly
 195 200 205

Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile
 210 215 220

Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly
 225 230 235 240

Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val
 245 250 255

Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg
 260 265 270

Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp
 275 280 285

Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp
 290 295 300

Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu
 305 310 315 320

Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg
 325 330 335

Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala
 340 345 350

Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro
 355 360 365

Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro

370

375

380

Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro
 385 390 395 400

Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro
 405 410 415

Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala
 420 425 430

Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His
 435 440 445

Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser
 450 455 460

Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr
 465 470 475 480

Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala
 485 490 495

Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His
 500 505 510

Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile
 515 520 525

Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
 530 535 540

Ser
 545

<210> 9
 <211> 552
 <212> PRT
 <213> Murine

<400> 9

Met Ala Gly Gly Asp Gly Met Leu Arg Arg Leu Leu Arg Leu His Arg
 1 5 10 15

Thr Glu Ile Ala Val Ala Ile Asp Ser Ala Phe Pro Leu Leu His Ala
 20 25 30

Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu
 35 40 45

Arg Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu
 50 55 60

Ser Trp Leu Leu Thr Arg Asp Ser Gly Ala Ile Leu Asp Phe Trp Arg
 65 70 75 80

Ile Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Ser Arg Leu His Ser
 85 90 95

Ile Leu Asp Gly Phe Pro Lys Asp Val Asp Leu Asn Gln Ser Arg Lys
 100 105 110

Gly Arg Lys Pro Leu Ala Gly Pro Lys Ala Ala Val Leu Pro Pro Arg
 115 120 125

Pro Pro Thr Lys Arg Lys Ala Leu Glu Glu Pro Arg Ala Thr Pro Pro
 130 135 140

Ala Thr Leu Ala Ser Lys Ser Val Ser Ser Pro Gly Ser His Leu Lys
 145 150 155 160

Thr Lys Pro Pro Lys Lys Pro Asp Gly Asn Leu Glu Ser Gln His Leu
 165 170 175

Pro Leu Gly Asn Gly Ile Gln Thr Met Ala Ala Ser Val Gln Arg Ala
 180 185 190

Val Thr Val Ala Ser Gly Asp Val Pro Gly Thr Arg Gly Ala Val Glu
 195 200 205

Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Arg Ser Lys Lys Cys
 210 215 220

Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Asn Lys Phe Glu Asp Pro
 225 230 235 240

Ser Gly Asn Leu Lys Asn Lys Ala Arg Ser Gly Ser Ser Leu Lys Pro
 245 250 255

Val Val Arg Ala Lys Gly Ala Gln Val Thr Ile Pro Gly Arg Asp Glu
 260 265 270

Gln Lys Val Gly Gln Gln Cys Gly Val Pro Pro Leu Pro Ser Leu Pro
 275 280 285

Ser Glu Pro Gln Val Asn Gln Lys Asn Glu Asp Glu Cys Ala Val Cys
 290 295 300

His Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe
 305 310 315 320

His Leu Ala Cys Leu Ser Pro Pro Leu Gln Glu Ile Pro Ser Gly Leu
 325 330 335

Trp Arg Cys Ser Cys Cys Leu Gln Gly Arg Val Gln Gln Asn Leu Ser
 340 345 350

Gln Pro Glu Val Ser Arg Pro Pro Glu Leu Pro Ala Glu Thr Pro Ile
 355 360 365

Leu Val Gly Leu Arg Ser Ala Ser Glu Lys Thr Arg Gly Pro Ser Arg
 370 375 380

Glu Leu Lys Ala Ser Ser Asp Ala Ala Val Thr Tyr Val Asn Leu Leu
 385 390 395 400

Ala Pro His Pro Ala Ala Pro Leu Leu Glu Pro Ser Ala Leu Cys Pro
 405 410 415

Leu Leu Ser Ala Gly Asn Glu Gly Arg Pro Gly Pro Ala Pro Ser Ala
 420 425 430

Arg Cys Ser Val Cys Gly Asp Gly Thr Glu Val Leu Arg Cys Ala His
 435 440 445

Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Thr Ala Ala Ala
 450 455 460

Arg Pro Gly Thr Asn Leu Arg Cys Lys Ser Cys Ser Ala Asp Ser Thr
 465 470 475 480

Pro Thr Pro Gly Thr Pro Gly Glu Ala Val Pro Thr Ser Gly Pro Arg
 485 490 495

Pro Ala Pro Gly Leu Ala Lys Val Gly Asp Asp Ser Ala Ser His Asp
 500 505 510

Pro Val Leu His Arg Asp Asp Leu Glu Ser Leu Leu Asn Glu His Ser

515

520

525

Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Ser Arg Pro Leu
 530 535 540

Ala Glu Thr Pro Pro Phe Ser Ser
 545 550

<210> 10
 <211> 550
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence of SEQ ID NO:8 & SEQ ID NO:10

<220>
 <221> MISC_FEATURE
 <222> (1)..(550)
 <223> Xaa denotes mismatch of SEQ ID NO:8 & SEQ ID NO:9

<400> 10

Xaa Xaa Xaa Asp Xaa Xaa Leu Arg Arg Leu Leu Arg Leu His Arg Thr
 1 5 10 15

Glu Ile Ala Val Ala Xaa Asp Ser Ala Phe Pro Leu Leu His Ala Leu
 20 25 30

Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu Xaa
 35 40 45

Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
 50 55 60

Trp Leu Leu Thr Xaa Asp Ser Xaa Ala Ile Leu Asp Phe Trp Arg Xaa
 65 70 75 80

Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Xaa Arg Leu Xaa Xaa Ile
 85 90 95

Leu Asp Xaa Phe Pro Lys Asp Val Asp Leu Xaa Gln Xaa Arg Lys Gly
 100 105 110

Arg Lys Pro Xaa Ala Xaa Pro Lys Ala Xaa Val Xaa Pro Pro Arg Xaa
 115 120 125

Pro Thr Lys Arg Lys Ala Xaa Glu Glu Xaa Arg Ala Xaa Xaa Pro Ala
 130 135 140

Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Ser Pro Gly Ser Xaa Leu Lys Xaa
 145 150 155 160

Lys Pro Pro Lys Lys Pro Xaa Xaa Xaa Xaa Glu Xaa Gln Xaa Leu Pro
 165 170 175

Leu Gly Asn Gly Ile Gln Thr Met Xaa Ala Ser Val Gln Arg Ala Val
 180 185 190

Xaa Xaa Xaa Ser Gly Asp Val Pro Gly Xaa Arg Gly Ala Val Glu Gly
 195 200 205

Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Xaa Ser Lys Lys Cys Ile
 210 215 220

Gln Val Gly Gly Glu Phe Tyr Thr Pro Xaa Lys Phe Glu Asp Xaa Ser
 225 230 235 240

Gly Xaa Xaa Lys Asn Lys Ala Arg Ser Xaa Ser Xaa Xaa Lys Pro Xaa
 245 250 255

Val Arg Ala Lys Gly Ala Gln Xaa Xaa Xaa Pro Gly Xaa Xaa Glu Xaa
 260 265 270

Xaa Xaa Gly Gln Gln Xaa Xaa Val Pro Xaa Xaa Xaa Xaa Leu Pro Ser
 275 280 285

Xaa Pro Gln Xaa Xaa Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Xaa
 290 295 300

Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His
 305 310 315 320

Leu Ala Cys Leu Ser Pro Pro Leu Xaa Glu Ile Pro Ser Gly Xaa Trp
 325 330 335

Arg Cys Ser Xaa Cys Leu Gln Xaa Xaa Val Gln Xaa Xaa Xaa Xaa Xaa
 340 345 350

Xaa Glu Xaa Xaa Arg Pro Xaa Glu Xaa Pro Xaa Glu Thr Pro Xaa Xaa
 355 360 365

Xaa Gly Leu Arg Ser Ala Xaa Glu Xaa Xaa Arg Gly Pro Xaa Xaa Glu
 370 375 380

Xaa Xaa Ala Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Xaa Xaa Leu Xaa Ala
 385 390 395 400

Pro Xaa Xaa Ala Ala Pro Leu Xaa Xaa Leu Xaa Xaa Ser Ala Leu Xaa
 405 410 415

Pro Leu Leu Xaa Xaa Gly Xaa Glu Gly Xaa Xaa Xaa Xaa Ala Pro Xaa
 420 425 430

Ala Arg Cys Xaa Val Cys Gly Asp Gly Thr Xaa Val Leu Arg Cys Xaa
 435 440 445

His Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Xaa Xaa Xaa
 450 455 460

Xaa Arg Pro Gly Thr Xaa Leu Arg Cys Xaa Ser Cys Ser Xaa Asp Xaa
 465 470 475 480

Thr Pro Xaa Pro Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Ser Xaa Xaa
 485 490 495

Arg Xaa Ala Pro Gly Xaa Ala Lys Xaa Xaa Asp Asp Xaa Ala Ser His
 500 505 510

Xaa Pro Xaa Leu His Arg Asp Asp Leu Glu Ser Leu Leu Xaa Glu His
 515 520 525

Xaa Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Xaa Arg Pro
 530 535 540

Xaa Ala Xaa Xaa Pro Xaa
 545 550

<210> 11
 <211> 48
 <212> DNA
 <213> Mouse

<400> 11
 ggggcctcga tggacgtctc tggggcccag gtcgtggttc gcgcgcta

48

<210> 12
 <211> 15
 <212> PRT
 <213> Mouse

<400> 12

Pro Glu Leu Pro Ala Glu Thr Pro Gly Pro Ala Pro Ser Ala Arg

1 5 10 15

<210> 13
 <211> 43
 <212> DNA
 <213> Mouse

<400> 13
 agtgagcccc aggttaacca gaacgaggat gagtgtgccg tgt 43

<210> 14
 <211> 14
 <212> PRT
 <213> Mouse

<400> 14
 Ser Glu Pro Gln Val Asn Gln Asn Glu Asp Glu Cys Ala Val
 1 5 10

<210> 15
 <211> 48
 <212> DNA
 <213> Mouse

<400> 15
 gtcaccaggc tcggttcctt cgggtcccat ctctactcgt ctttcacc 48

<210> 16
 <211> 15
 <212> PRT
 <213> Mouse

<400> 16
 Val Val Arg Ala Lys Gly Ala Gln Gly Arg Asp Glu Gln Lys Val
 1 5 10 15

<210> 17
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 17
 agaagtgcac ccaggttggc 20

<210> 18
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>

<223> PCR primer

<400> 18
ggaagagggg cgtcagcaat

20

<210> 19
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 19

Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg
1 5 10 15

<210> 20
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 20

Ser Gln Pro Arg Lys Gly Arg Lys Pro Pro Ala Val Pro Lys
1 5 10

<210> 21
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> B127FR4-29 primer for PCR

<400> 21
gctctggatg gcctactgc

19

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> B127FR4-17 primer for PCR

<400> 22
agaagtgcac ccagggtggc

20

<210> 23
<211> 19
<212> DNA

<213> Artificial Sequence

<220>

<223> B127FR4-33 primer for PCR

<400> 23

gtgtgctcgc tcagaaggg

19

<210> 24

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward primer Mforw4 for PCR

<400> 24

tggcaggtgg ggatggaa

18

<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse primer Mrev15 for PCR

<400> 25

ggagggatgg aaggggagga

20

<210> 26

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward primer Mforw2 for PCR

<400> 26

tcccacctga agactaagc

19

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse primer Mrev32 for PCR

<400> 27

tcacagctct ctggacagaa

20

<210> 28

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer B127FR4-21 for PCR

<400> 28

ggcttctgag gctgcacc

18

<210> 29

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Double-paired finger motif

<400> 29

Cys Cys Cys Cys His Cys Cys Cys
1 5

<210> 30

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Structural motiff

<220>

<221> MISC_FEATURE

<222> (1)..(42)

<223> Xaa is any amino acid

<400> 30

Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
1 5 10 15

Xaa Xaa Xaa Xaa His Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
35 40